



568.1D1.TXT

SEQUENCE LISTING

<110> Madison, Edwin L

<120> TISSUE TYPE PLASMINOGEN ACTIVATOR (t-PA)
VARIANTS: COMPOSITIONS AND METHODS OF USE

<130> TSRI 568.1D1

<140> US 10/705,633

<141> 2003-11-10

<150> US 09/600,985

<151> 2000-11-13

<150> PCT/US97/20226

<151> 1997-11-12

<150> US 60/030,655

<151> 1996-11-12

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 527

<212> PRT

<213> Homo sapiens

<400> 1

Ser	Tyr	Gln	Val	Ile	Cys	Arg	Asp	Glu	Lys	Thr	Gln	Met	Ile	Tyr	Gln
1				5					10					15	
Gln	His	Gln	Ser	Trp	Leu	Arg	Pro	Val	Leu	Arg	Ser	Asn	Arg	Val	Glu
			20					25					30		
Tyr	Cys	Trp	Cys	Asn	Ser	Gly	Arg	Ala	Gln	Cys	His	Ser	Val	Pro	Val
			35				40					45			
Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Gln	Gln
	50					55					60				
Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu	Gly	Phe	Ala
65					70				75					80	
Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr	Glu	Asp	Gln
				85					90					95	
Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	Gly	Ala	Glu
			100					105					110		
Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	Tyr	Ser	Gly
		115					120					125			
Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	Asn	Tyr	Cys
		130				135					140				
Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	Phe	Lys	Ala
145					150					155					160
Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	Ser	Glu	Gly
				165					170					175	
Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	Gly	Thr	His
			180					185					190		
Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	Ser	Met	Ile
		195					200						205		

568.1D1.TXT

```

Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
210                215                220
Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
225                230                235
Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
245                250                255
Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
260                265                270
Gln Phe Glu Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
275                280                285
Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
290                295                300
Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
305                310                315
Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
325                330                335
Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
340                345                350
Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
355                360                365
Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
370                375                380
Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
385                390                395
Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
405                410                415
Asp Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
420                425                430
Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
435                440                445
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
450                455                460
Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
465                470                475
Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
485                490                495
Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
500                505                510
Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro
515                520                525

```

<210> 2

<211> 527

<212> PRT

<213> Homo sapiens

<400> 2

```

Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
1          5          10          15
Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
20          25          30
Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
35          40          45
Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
50          55          60
Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
65          70          75          80
Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln

```

568.1D1.TXT

										85											90											95	
Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	Gly	Ala	Glu																		
			100						105																								
Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	Tyr	Ser	Gly																		
			115						120																								
Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	Asn	Tyr	Cys																		
			130						135																								
Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	Phe	Lys	Ala																		
			145						150																								
Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	Ser	Glu	Gly																		
			165						170																								
Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	Gly	Thr	His																		
			180						185																								
Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	Ser	Met	Ile																		
			195						200																								
Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	Gln	Ala	Leu																		
			210						215																								
Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ala	Lys																		
			225						230																								
Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	Glu	Tyr	Cys																		
			245						250																								
Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	Ser	Gln	Pro																		
			260						265																								
Gln	Phe	Glu	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala	Ser	His	Pro																		
			275						280																								
Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro	Gly	Glu	Arg																		
			290						295																								
Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile	Leu	Ser	Ala																		
			305						310																								
Ala	His	Cys	Phe	Gln	Glu	Arg	Phe	Pro	Pro	His	His	Leu	Thr	Val	Ile																		
			325						330																								
Leu	Gly	Arg	Thr	Tyr	Arg	Val	Val	Pro	Gly	Glu	Glu	Glu	Gln	Lys	Phe																		
			340						345																								
Glu	Val	Glu	Lys	Tyr	Ile	Val	His	Lys	Glu	Phe	Asp	Asp	Asp	Thr	Tyr																		
			355						360																								
Asp	Asn	Asp	Ile	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Asp	Ser	Ser	Arg	Cys																		
			370						375																								
Ala	Gln	Glu	Ser	Ser	Val	Val	Arg	Thr	Val	Cys	Leu	Pro	Pro	Ala	Asp																		
			385						390																								
Leu	Gln	Leu	Pro	Asp	Trp	Thr	Glu	Cys	Glu	Leu	Ser	Gly	Tyr	Gly	Lys																		
			405						410																								
Glu	Glu	Ala	Leu	Ser	Pro	Phe	Tyr	Ser	Glu	Arg	Leu	Lys	Glu	Ala	His																		
			420						425																								
Val	Arg	Leu	Tyr	Pro	Ser	Ser	Arg	Cys	Thr	Ser	Gln	His	Leu	Leu	Asn																		
			435						440																								
Arg	Thr	Val	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Asp	Thr	Arg	Ser	Gly																		
			450						455																								
Gly	Pro	Gln	Ala	Asn	Leu	His	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly																		
			465						470																								
Pro	Leu	Val	Cys	Leu	Asn	Asp	Gly	Arg	Met	Thr	Leu	Val	Gly	Ile	Ile																		
			485						490																								
Ser	Trp	Gly	Leu	Gly	Cys	Gly	Gln	Lys	Asp	Val	Pro	Gly	Val	Tyr	Thr																		
			500						505																								
Lys	Val	Thr	Asn	Tyr	Leu	Asp	Trp	Ile	Arg	Asp	Asn	Met	Arg	Pro																			
			515						520																								

<210> 3
 <211> 527

<212> PRT

<213> Homo sapiens

<400> 3

```

Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
 1           5           10           15
Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
 20           25           30
Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
 35           40           45
Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
 50           55           60
Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
 65           70           75           80
Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
 85           90           95
Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
 100          105          110
Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
 115          120          125
Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
 130          135          140
Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
 145          150          155          160
Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
 165          170          175
Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
 180          185          190
Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
 195          200          205
Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
 210          215          220
Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
 225          230          235          240
Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
 245          250          255
Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
 260          265          270
Gln Phe Glu Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
 275          280          285
Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
 290          295          300
Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
 305          310          315          320
Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
 325          330          335
Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
 340          345          350
Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
 355          360          365
Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
 370          375          380
Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
 385          390          395          400
Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
 405          410          415
His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Tyr Glu Ala His
 420          425          430
Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn

```

568.1D1.TXT

		435					440					445				
Arg	Thr	Val	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Asp	Thr	Arg	Ser	Gly	
	450					455					460					
Gly	Pro	Gln	Ala	Asn	Leu	His	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	
465					470					475					480	
Pro	Leu	Val	Cys	Leu	Asn	Asp	Gly	Arg	Met	Thr	Leu	Val	Gly	Ile	Ile	
				485				490						495		
Ser	Trp	Gly	Leu	Gly	Cys	Gly	Gln	Lys	Asp	Val	Pro	Gly	Val	Tyr	Thr	
			500					505					510			
Lys	Val	Thr	Asn	Tyr	Leu	Asp	Trp	Ile	Arg	Asp	Asn	Met	Arg	Pro		
		515					520					525				

```
<210> 4
<211> 290
<212> DNA
<213> Homo sapiens
```

<400>	4						
ctacggcaag	catgaggcct	tgtctccttt	ctattcggag	cggctgaagg	aggctcatgt	60	
cagactgtac	ccatccagcc	gctgcacatc	acaacattta	cttaacagaa	cagtcaccga	120	
caacatgctg	tgtgctggag	acactcggag	cggcggtccc	caggcaaac	tgcacgacgc	180	
ctgccagggc	gattcgggag	gccccctggt	gtgctggaac	gatggccgca	tgactttggt	240	
gggcatcatc	agctggggcc	tgggctgtgg	acagaaggat	gtcccggtg		290	

```
<210> 5
<211> 290
<212> DNA
<213> Homo sapiens
```

<400> 5						
ctacggcaag	gacgaggcct	tgtctccttt	ctattcggag	cggctgaagg	aggctcatgt	60
cagactgtac	ccatccagcc	gctgcacatc	acaacattta	cttaacagaa	cagtcaccga	120
caacatgctg	tgtgctggag	acactcggag	cggcgcgccc	caggcaaact	tgcacgacgc	180
ctgccaggcg	gattcgggag	gccccctggt	gtgtctgaac	gatggccgca	tgactttggt	240
gggcatcadc	agctggggcc	tgggctgtgg	acagaaggat	gtcccggtg		290

```
<210> 6
<211> 290
<212> DNA
<213> Homo sapiens
```

<400> 6						
ctacggcaag	gaggaggcct	tgtctccttt	ctattcggag	cggctgaagg	aggctcatgt	60
cagactgtac	ccatccagcc	gctgcacatc	acaacattta	cttaacagaa	cagtcaccga	120
caacatgctg	tgtgctggag	acactcggag	cggcggtgcc	caggcaaact	tgcacgacgc	180
ctgccagggc	gattcgggag	gccccctggt	gtgctggaac	gatggccgca	tgactttggt	240
gggcatcadc	agctggggcc	tgggctgtgg	acagaaggat	gtcccggttg		290

```
<210> 7
<211> 290
<212> DNA
<213> Homo sapiens
```

<400> 7						
ctacggcaag	catgaggcct	tgtctccttt	ctatttcggag	cggctgtatg	aggctcatgt	60
cagactgtac	ccatccagcc	gctgcacatc	acaacattta	cttaacagaa	cagtcaccga	120
caacatgctg	tgtgctggag	acactcggag	cggcggggcc	caggcaaaat	tgcacgacgc	180
ctgccagggc	gattcgggaq	gcctccctggt	gtgtctgaac	gatggccqca	tgaactttggt	240

```

gggcatcatc agctggggcc tgggctgtgg acagaaggat gtcccgggtg      290
<210> 8
<211> 23
<212> DNA
<213> Homo sapiens

<400> 8
ctacggcaag gacgaggcct tgt      23

<210> 9
<211> 23
<212> DNA
<213> Homo sapiens

<400> 9
ctacggcaag gaggaggcct tgt      23

<210> 10
<211> 26
<212> DNA
<213> Homo sapiens

<400> 10
cggagcggct gtatgaggct mcatgt      26

<210> 11
<211> 2544
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (86)...(1774)

<221> sig_peptide
<222> (86)...(190)

<400> 11
gttctgagca cagggctgga gagaaaacct ctgcgaggaa agggaaggag caagccgtga 60
atttaaggga cgctgtgaag caatc atg gat gca atg aag aga ggg ctc tgc 112
                Met Asp Ala Met Lys Arg Gly Leu Cys
                -35                      -30

tgt gtg ctg ctg ctg tgt gga gca gtc ttc gtt tcg ccc agc cag gaa 160
Cys Val Leu Leu Leu Cys Gly Ala Val Phe Val Ser Pro Ser Gln Glu
-25                      -20                      -15

atc cat gcc cga ttc aga aga gga gcc aga tct tac caa gtg atc tgc 208
Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr Gln Val Ile Cys
-10                      -5                      1                      5

aga gat gaa aaa acg cag atg ata tac cag caa cat cag tca tgg ctg 256
Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp Leu
10                      15                      20

cgc cct gtg ctc aga agc aac cgg gtg gaa tat tgc tgg tgc aac agt 304
Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser
25                      30                      35

```

568.1D1.TXT

```

ggc agg gca cag tgc cac tca gtg cct gtc aaa agt tgc agc gag cca 352
Gly Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro
40 45 50

agg tgt ttc aac ggg ggc acc tgc cag cag gcc ctg tac ttc tca gat 400
Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp
55 60 65 70

ttc gtg tgc cag tgc ccc gaa gga ttt gct ggg aag tgc tgt gaa ata 448
Phe Val Cys Gln Cys Pro Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile
75 80 85

gat acc agg gcc acg tgc tac gag gac cag ggc atc agc tac agg ggc 496
Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln Gly Ile Ser Tyr Arg Gly
90 95 100

acg tgg agc aca gcg gag agt ggc gcc gag tgc acc aac tgg aac agc 544
Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys Thr Asn Trp Asn Ser
105 110 115

agc gcg ttg gcc cag aag ccc tac agc ggg cgg agg cca gac gcc atc 592
Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp Ala Ile
120 125 130

agg ctg ggc ctg ggg aac cac aac tac tgc aga aac cca gat cga gac 640
Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
135 140 145 150

tca aag ccc tgg tgc tac gtc ttt aag gcg ggg aag tac agc tca gag 688
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu
155 160 165

ttc tgc agc acc cct gcc tgc tct gag gga aac agt gac tgc tac ttt 736
Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe
170 175 180

ggg aat ggg tca gcc tac cgt ggc acg cac agc ctc acc gag tcg ggt 784
Gly Asn Gly Ser Ala Tyr Arg Gly Thr His Ser Leu Thr Glu Ser Gly
185 190 195

gcc tcc tgc ctc ccg tgg aat tcc atg atc ctg ata ggc aag gtt tac 832
Ala Ser Cys Leu Pro Trp Asn Ser Met Ile Leu Ile Gly Lys Val Tyr
200 205 210

aca gca cag aac ccc agt gcc cag gca ctg ggc ctg ggc aaa cat aat 880
Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu Gly Lys His Asn
215 220 225 230

tac tgc cgg aat cct gat ggg gat gcc aag ccc tgg tgc cac gtg ctg 928
Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His Val Leu
235 240 245

aag aac cgc agg ctg acg tgg gag tac tgt gat gtg ccc tcc tgc tcc 976
Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
250 255 260

acc tgc ggc ctg aga cag tac agc cag cct cag ttt cgc atc aaa gga 1024
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly

```

568.1D1.TXT

265	270	275	
ggg ctc ttc gcc gac atc gcc tcc cac ccc tgg cag gct gcc atc ttt Gly Leu Phe Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe 280 285 290			1072
gcc aag cac agg agg tcg ccc gga gag cgg ttc ctg tgc ggg ggc ata Ala Lys His Arg Arg Ser Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile 295 300 305 310			1120
ctc atc agc tcc tgc tgg att ctc tct gcc gcc cac tgc ttc cag gag Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala Ala His Cys Phe Gln Glu 315 320 325			1168
agg ttt ccg ccc cac cac ctg acg gtg atc ttg ggc aga aca tac cgg Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg 330 335 340			1216
gtg gtc cct ggc gag gag gag cag aaa ttt gaa gtc gaa aaa tac att Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile 345 350 355			1264
gtc cat aag gaa ttc gat gat gac act tac gac aat gac att gcg ctg Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu 360 365 370			1312
ctg cag ctg aaa tcg gat tcg tcc cgc tgt gcc cag gag agc agc gtg Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val 375 380 385 390			1360
gtc cgc act gtg tgc ctt ccc ccg gcg gac ctg cag ctg ccg gac tgg Val Arg Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp 395 400 405			1408
acg gag tgt gag ctc tcc ggc tac ggc aag cat gag gcc ttg tct cct Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro 410 415 420			1456
ttc tat tcg gag cgg ctg aag gag gct cat gtc aga ctg tac cca tcc Phe Tyr Ser Glu Arg Leu Lys Glu Ala His Val Arg Leu Tyr Pro Ser 425 430 435			1504
agc cgc tgc aca tca caa cat tta ctt aac aga aca gtc acc gac aac Ser Arg Cys Thr Ser Gln His Leu Leu Asn Arg Thr Val Thr Asp Asn 440 445 450			1552
atg ctg tgt gct gga gac act cgg agc ggc ggg ccc cag gca aac ttg Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu 455 460 465 470			1600
cac gac gcc tgc cag ggc gat tcg gga ggc ccc ctg gtg tgt ctg aac His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Asn 475 480 485			1648
gat ggc cgc atg act ttg gtg ggc atc atc agc tgg ggc ctg ggc tgt Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys 490 495 500			1696
gga cag aag gat gtc ccg ggt gtg tac acc aag gtt acc aac tac cta			1744

568.1D1.TXT

Gly Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu
 505 510 515

gac tgg att cgt gac aac atg cga ccg tga ccaggaacac ccgactcctc 1794
 Asp Trp Ile Arg Asp Asn Met Arg Pro *
 520 525

aaaagcaaat gagatcccgc ctcttcttct tcagaagaca ctgcaaaggc gcagtgtctc 1854
 tctacagact tctccagacc caccacaccg cagaagcggg acgagaccct acaggagagg 1914
 gaagagtgc ttttcccaga tacttcccat tttggaagtt ttcaggactt ggtctgattt 1974
 caggatactc tgtcagatgg gaagacatga atgcacacta gcctctccag gaatgcctcc 2034
 tccctgggca gaaagtggcc atgccaccct gttttcagct aaagcccaac ctcttgacct 2094
 gtcaccgtga gcagctttgg aaacaggacc acaaaaatga aagcatgtct caatagtaaa 2154
 agataacaag atctttcagg aaagacggat tgcattagaa atagacagta tatttatagt 2214
 cacaagagcc cagcagggcc tcaaagttgg ggcaggctgg ctggcccgtc atgttcctca 2274
 aaagcaccct tgacgtcaag tctccttccc ctttcccccac tccctggctc tcagaaggta 2334
 ttccttttgg gtacagtgtg taaagtgtaa atcctttttc tttataaact ttagagtagc 2394
 atgagagaat tgtatcattt gaacaactag gcttcagcat atttatagca atccatgtta 2454
 gtttttactt tctgttgcca caaccctgtt ttatactgta cttaataaat tcagatatat 2514
 ttttcacagt ttttcacaaa aaaaaaaaaa 2544

<210> 12
 <211> 562
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(35)

<400> 12
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 -35 -30 -25 -20
 Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
 -15 -10 -5
 Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
 1 5 10
 Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
 15 20 25
 Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
 30 35 40 45
 Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
 50 55 60
 Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
 65 70 75
 Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
 80 85 90
 Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
 95 100 105
 Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
 110 115 120 125
 Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
 130 135 140
 Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
 145 150 155
 Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
 160 165 170
 Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
 175 180 185

Trial	Control (n = 10)	MCI (n = 10)	AD (n = 10)
1	95	85	75
2	95	85	75
3	95	80	70
4	95	75	65
5	95	75	65

[illegible]